Fecal contamination hotspots in low-income households in Bangladesh

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specific domains of ICATB evaluation: 18.2% of HCIs does not have a Committee for AMS. Antimicrobial use surveillance is performed by 84.9% of HCIs, but only 36.4% audits on antimicrobial prescription. While only 54.6% of HCIs have some kind of digital records, 45.5% have computer-based prescription. Only 39.4% have education of new prescribers; and 45.5% have restrictions on antimicrobial prescription.

Conclusion: Large HCIs in Argentina have a fair AMS performance. However, we observed improvement opportunities for Information Technology. Half of the HCIs evaluated have not implemented any kind of digital AMS, and a complete computerization could be beneficial to facilitate activities and to improve data analysis to have a better impact on AMS. Educational activities should also be improved by the HCIs. Further studies are needed to evaluate the impact of these programs on optimization of antimicrobial use and resistance and health care outcomes, including mortality and costs in Argentina.

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Fecal contamination hotspots in low-income households in Bangladesh

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Background: Diarrheal diseases continue to be major causes of morbidity and mortality in developing countries. Infectious Diarrhea is often related to fecal pathogen exposure via drinking water. Little is known about the other fecal contamination hotspots within the household and especially in the kitchen environments in overcrowded low-income setting. Current study intended to perform quantitative analysis of fecal contamination in food and domestic surfaces.

Methods & Materials: Fecal contamination was surveyed in routine swabs from four household environmental sites: cutting knife (n = 169), food plate (n = 165), latrine door knob (n = 169), and drinking water pot surface (n = 165) among 32 households for 1 year period in a low-income area, Arichpur, Dhaka. Moreover, 137 left over food samples were taken. All the samples were analysed for total thermotolerant *Escherichia coli* count and the presence of *Vibrio cholerae* by molecular method. Fisher's exact test was used to compare the fecal contamination level in different surface locations. A subset of samples was assessed for the genomic presence of diarrheagenic *E. coli* by PCR.

Results: Results revealed that *E. coli* contamination level was highest on food plates with a geometric mean (GM) of 3.08 cfu/cm^2 and the least contaminated site was latrine door knob (GM = 0.06 cfu/cm^2). Food samples were found heavily contaminated with fecal *E. coli* (GM = 13.32 cfu/gm, with counts ranges from 0 to 6400 cfu/gm). The level of fecal contamination is 4.7 times higher ($p < 0.05$) in cutting knife than latrine door knob surfaces and 0.3 times lower ($p < 0.05$) in latrine door knob than drinking water pot surfaces. *V. cholerae* contamination was also most predominant in food plate swabs. Genes of enterotoxigenic *E. coli* (ETEC), enterohaemorrhagic *E. coli* (EHEC) and enteropathogenic *E. coli* (EPEC) were detected in surface samples among them ETEC was the most prevalent (46% samples were found positive).

Conclusion: This study presents new dynamics of in-house components in transmission of fecal bacteria via food and kitchen utensils thus, proves the vulnerability of the kitchen environment of low-income urban settings in Bangladesh. Results of the study will enable an update of the diarrhea risk factors for early prevention of disease progression in risk groups.

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Gastrointestinal colonization by vanA glycopeptide resistant Enterococcus species harbouring multiple virulence genes in western Nepal

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Background: Gastrointestinal colonization by vancomycin resistant *Enterococcus* (VRE) has regularly been reported worldwide. Fecal carriage rate and virulence properties of such colonisers have not been established so far in context to Nepal. This study was conducted to address these prevailing issues.

Methods & Materials: Rectal swabs were screened for multi drug resistant (MDR) *Enterococcus* species. MICs of vancomycin and teicoplanin were determined by E- test. VRE isolates were further investigated for various pathogenic markers. Pulsed field gel electrophoresis (PFGE) was used to investigate the genetic relatedness between VRE strains. *Drosophila melanogaster* insect model was used to determine the colonisation capability and virulence of VRE.

Results: Of the 270 subjects studied, 142 (52.59%) yielded *Enterococci* spp. Forty seven (33.1%) out of 142 *Enterococci* were MDR. 31 (72.1%) of 43 hospitalizes individuals were colonised with MDR *Enteroccocci*, as compared to only 16 (16.2%) of 99 community individuals ($\chi^2 = 42.35$; $p < 0.001$). We found that 18.6% (8/43) of the hospitalised patients and 1.01% (1/99) community subjects was colonised with VRE, ($\chi^2 = 15.63$; $p < 0.001$), faecal colony counts ranging between 10^2 to 10^4 CFU/gm. Seven VRE isolates were identified as *E faecium* and two as *E faecalis.* All the isolates belonged to vanA genotype. *In vitro* virulence determinants such as biofilm production, extracellular enzymatic and haemolytic activities were absent, despite all the strains possessing multiple virulence genes like *esp*, *asa1 gelE*, *ace*, *hyl*, *cylA*, *cpd* and *ebpA* and being capable of producing slime. PFGE analysis revealed two different traits of which, majority (6/9) had the same clonal origin. None of the VRE isolates were capable of gut colonization or causing death in *Drosophila* during the 10 days study period as assessed by fly feeding experiment. Mean VRE concentrations in the gut of flies